

RAW SEQUENCE LISTING

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Application Serial Number: 10/771,833A
Source: JFW16
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IFW16

RAW SEQUENCE LISTING

DATE: 11/24/2006

PATENT APPLICATION: US/10/771,833A

TIME: 14:27:16

Input Set : A:\39363106.APP

Output Set: N:\CRF4\11242006\J771833A.raw

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3 <110> APPLICANT: ARTIS, DEAN R.
4     BOLLAG, GIDEON
5     CARD, GRAEME
6     MARTIN, FERNANDO
7     MILBURN, MICHAEL V.
8     ZHANG, KAM
10 <120> TITLE OF INVENTION: PDE5A CRYSTAL STRUCTURE AND USES
12 <130> FILE REFERENCE: 039363-1106
14 <140> CURRENT APPLICATION NUMBER: 10/771,833A
15 <141> CURRENT FILING DATE: 2004-02-03
17 <150> PRIOR APPLICATION NUMBER: 60/485,627
18 <151> PRIOR FILING DATE: 2003-07-07
20 <150> PRIOR APPLICATION NUMBER: 60/444,734
21 <151> PRIOR FILING DATE: 2003-02-03
23 <160> NUMBER OF SEQ ID NOS: 34
25 <170> SOFTWARE: PatentIn Ver. 3.3
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 875
29 <212> TYPE: PRT
30 <213> ORGANISM: Homo sapiens
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36 Pro Gln Gln Gln Lys Gln Gln Gln Arg Asp Gln Asp Ser Val Glu Ala
37               20               25               30
39 Trp Leu Asp Asp His Trp Asp Phe Thr Phe Ser Tyr Phe Val Arg Lys
40   35               40               45
42 Ala Thr Arg Glu Met Val Asn Ala Trp Phe Ala Glu Arg Val His Thr
43   50               55               60
45 Ile Pro Val Cys Lys Glu Gly Ile Arg Gly His Thr Glu Ser Cys Ser
46   65               70               75               80
48 Cys Pro Leu Gln Gln Ser Pro Arg Ala Asp Asn Ser Val Pro Gly Thr
49               85               90               95
51 Pro Thr Arg Lys Ile Ser Ala Ser Glu Phe Asp Arg Pro Leu Arg Pro
52   100               105               110
54 Ile Val Val Lys Asp Ser Glu Gly Thr Val Ser Phe Leu Ser Asp Ser
55   115               120               125
57 Glu Lys Lys Glu Gln Met Pro Leu Thr Pro Pro Arg Phe Asp His Asp
58   130               135               140
60 Glu Gly Asp Gln Cys Ser Arg Leu Leu Glu Leu Val Lys Asp Ile Ser
61 145               150               155               160
63 Ser His Leu Asp Val Thr Ala Leu Cys His Lys Ile Phe Leu His Ile
64   165               170               175

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66 His Gly Leu Ile Ser Ala Asp Arg Tyr Ser Leu Phe Leu Val Cys Glu
67          180          185          190
69 Asp Ser Ser Asn Asp Lys Phe Leu Ile Ser Arg Leu Phe Asp Val Ala
70          195          200          205
72 Glu Gly Ser Thr Leu Glu Glu Val Ser Asn Asn Cys Ile Arg Leu Glu
73          210          215          220
75 Trp Asn Lys Gly Ile Val Gly His Val Ala Ala Leu Gly Glu Pro Leu
76 225          230          235          240
78 Asn Ile Lys Asp Ala Tyr Glu Asp Pro Arg Phe Asn Ala Glu Val Asp
79          245          250          255
81 Gln Ile Thr Gly Tyr Lys Thr Gln Ser Ile Leu Cys Met Pro Ile Lys
82          260          265          270
84 Asn His Arg Glu Glu Val Val Gly Val Ala Gln Ala Ile Asn Lys Lys
85          275          280          285
87 Ser Gly Asn Gly Gly Thr Phe Thr Glu Lys Asp Glu Lys Asp Phe Ala
88          290          295          300
90 Ala Tyr Leu Ala Phe Cys Gly Ile Val Leu His Asn Ala Gln Leu Tyr
91 305          310          315          320
93 Glu Thr Ser Leu Leu Glu Asn Lys Arg Asn Gln Val Leu Leu Asp Leu
94          325          330          335
96 Ala Ser Leu Ile Phe Glu Glu Gln Gln Ser Leu Glu Val Ile Leu Lys
97          340          345          350
99 Lys Ile Ala Ala Thr Ile Ile Ser Phe Met Gln Val Gln Lys Cys Thr
100          355          360          365
102 Ile Phe Ile Val Asp Glu Asp Cys Ser Asp Ser Phe Ser Ser Val Phe
103          370          375          380
105 His Met Glu Cys Glu Glu Leu Glu Lys Ser Ser Asp Thr Leu Thr Arg
106 385          390          395          400
108 Glu His Asp Ala Asn Lys Ile Asn Tyr Met Tyr Ala Gln Tyr Val Lys
109          405          410          415
111 Asn Thr Met Glu Pro Leu Asn Ile Pro Asp Val Ser Lys Asp Lys Arg
112          420          425          430
114 Phe Pro Trp Thr Thr Glu Asn Thr Gly Asn Val Asn Gln Gln Cys Ile
115          435          440          445
117 Arg Ser Leu Leu Cys Thr Pro Ile Lys Asn Gly Lys Lys Asn Lys Val
118          450          455          460
120 Ile Gly Val Cys Gln Leu Val Asn Lys Met Glu Glu Asn Thr Gly Lys
121 465          470          475          480
123 Val Lys Pro Phe Asn Arg Asn Asp Glu Gln Phe Leu Glu Ala Phe Val
124          485          490          495
126 Ile Phe Cys Gly Leu Gly Ile Gln Asn Thr Gln Met Tyr Glu Ala Val
127          500          505          510
129 Glu Arg Ala Met Ala Lys Gln Met Val Thr Leu Glu Val Leu Ser Tyr
130          515          520          525
132 His Ala Ser Ala Ala Glu Glu Thr Arg Glu Leu Gln Ser Leu Ala
133          530          535          540
135 Ala Ala Val Val Pro Ser Ala Gln Thr Leu Lys Ile Thr Asp Phe Ser
136 545          550          555          560
138 Phe Ser Asp Phe Glu Leu Ser Asp Leu Glu Thr Ala Leu Cys Thr Ile

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139          565          570          575
141 Arg Met Phe Thr Asp Leu Asn Leu Val Gln Asn Phe Gln Met Lys His
142          580          585          590
144 Glu Val Leu Cys Arg Trp Ile Leu Ser Val Lys Lys Asn Tyr Arg Lys
145          595          600          605
147 Asn Val Ala Tyr His Asn Trp Arg His Ala Phe Asn Thr Ala Gln Cys
148          610          615          620
150 Met Phe Ala Ala Leu Lys Ala Gly Lys Ile Gln Asn Lys Leu Thr Asp
151 625          630          635          640
153 Leu Glu Ile Leu Ala Leu Leu Ile Ala Ala Leu Ser His Asp Leu Asp
154          645          650          655
156 His Arg Gly Val Asn Asn Ser Tyr Ile Gln Arg Ser Glu His Pro Leu
157          660          665          670
159 Ala Gln Leu Tyr Cys His Ser Ile Met Glu His His His Phe Asp Gln
160          675          680          685
162 Cys Leu Met Ile Leu Asn Ser Pro Gly Asn Gln Ile Leu Ser Gly Leu
163          690          695          700
165 Ser Ile Glu Glu Tyr Lys Thr Thr Leu Lys Ile Ile Lys Gln Ala Ile
166 705          710          715          720
168 Leu Ala Thr Asp Leu Ala Leu Tyr Ile Lys Arg Arg Gly Glu Phe Phe
169          725          730          735
171 Glu Leu Ile Arg Lys Asn Gln Phe Asn Leu Glu Asp Pro His Gln Lys
172          740          745          750
174 Glu Leu Phe Leu Ala Met Leu Met Thr Ala Cys Asp Leu Ser Ala Ile
175          755          760          765
177 Thr Lys Pro Trp Pro Ile Gln Gln Arg Ile Ala Glu Leu Val Ala Thr
178          770          775          780
180 Glu Phe Phe Asp Gln Gly Asp Arg Glu Arg Lys Glu Leu Asn Ile Glu
181 785          790          795          800
183 Pro Thr Asp Leu Met Asn Arg Glu Lys Lys Asn Lys Ile Pro Ser Met
184          805          810          815
186 Gln Val Gly Phe Ile Asp Ala Ile Cys Leu Gln Leu Tyr Glu Ala Leu
187          820          825          830
189 Thr His Val Ser Glu Asp Cys Phe Pro Leu Leu Asp Gly Cys Arg Lys
190          835          840          845
192 Asn Arg Gln Lys Trp Gln Ala Leu Ala Glu Gln Gln Glu Lys Met Leu
193          850          855          860
195 Ile Asn Gly Glu Ser Gly Gln Ala Lys Arg Asn
196 865          870          875
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200 <211> LENGTH: 3106
201 <212> TYPE: DNA
202 <213> ORGANISM: Homo sapiens
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206 ggggtctcgag gccgagtcct gttcttctga gggacggacc ccagctgggg tggaaaagca 120
207 gtaccagaga gcctccgagg cgcgcggtgc caaccatgga gcgggccggc cccagcttcg 180
208 ggcagcagcg acagcagcag cagccccagc agcagaagca gcagcagagg gatcaggact 240
209 cggtcgaagc atggctggac gatcactggg actttacctt ctcatacttt gttagaaaag 300

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210 ccaccagaga aatggtcaat gcatgggtttg ctgagagagt tcacaccatc cctgtgtgca 360
211 aggaaggtat cagaggccac accgaatctt gctcttgccc cttgcagcag agtcctcgtg 420
212 cagataacag tgccctgga acaccaacca ggaaaatctc tgccctctgaa ttgaccggc 480
213 ctcttagacc cattgttgct aaggattctg agggaaactgt gagcttctc tctgactcag 540
214 aaaagaagga acagatgcct ctaaccctc caaggtttga tcatgatgaa ggggaccagt 600
215 gctcaagact cttggaatta gtgaaggata tttctagtca tttggatgtc acagccttat 660
216 gtcacaaaat tttcttgcat atccatggac tgatatctgc tgaccgctat tccctgttcc 720
217 ttgtctgtga agacagctcc aatgacaagt ttcttatcag ccgcctcttt gatgttgctg 780
218 aaggttcaac actggaagaa gtttcaaata actgtatccg cttagaatgg aacaaaggca 840
219 ttgtgggaca tgtggcagcg cttggtgagc ccttgaacat caaagatgca tatgaggatc 900
220 ctcggttcaa tgcagaagtt gaccaaatta caggctacaa gacacaaagc attctttgta 960
221 tgccaattaa gaatcatagg gaagagggtt ttggtgtagc ccaggccatc aacaagaaat 1020
222 caggaaacgg tgggacattt actgaaaaag atgaaaagga ctttgctgct tatttggcat 1080
223 tttgtggtat tgttcttcat aatgctcagc tctatgagac ttcactgctg gagaacaaga 1140
224 gaaatcaggt gctgcttgac cttgctagtt taatttttga agaacaacaa tcattagaag 1200
225 taattttgaa gaaaatagct gccactatta tctctttcat gcaagtgcag aaatgcacca 1260
226 ttttcatagt ggaatgaagt tgctccgatt ctttttctag tgtgtttcac atggagtgtg 1320
227 aggaattaga aaaatcatct gatacattaa caagggaaca tgatgcaaac aaaatcaatt 1380
228 acatgtatgc tcagtatgtc aaaaatacta tggaaacctc taatatccca gatgtcagta 1440
229 aggataaaaag atttccttgg acaactgaaa atacaggaaa tgtaaaccag cagtgcatta 1500
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249 atgaggccct gaccacgtg tcagaggact gtttcccttt gctagatggc tgcagaaaga 2700
250 acaggcagaa atggcaggcc cttgcagaac agcaggagaa gatgctgatt aatggggaaa 2760
251 gcggccaggc caagcggaac tgagtggcct atttcatgca gagttgaagt ttacagagat 2820
252 ggtgtgttct gcaatatgcc tagttttctta cactactgtc gtatagtgtc tgtatttggg 2880
253 atatactttg cactgctgt atttttattt ttgcacaact tttgagagta tagcatgaat 2940
254 gtttttagag gactattaca tattttttgt atatttgttt tatgctactg aactgaaagg 3000
255 atcaacaaca tccactgtta gcacattgat aaaagcattg tttgtgatat ttcgtgtact 3060
256 gcaaagtgtg tgcagtattc ttgcactgag gtttttttgc ttggggg 3106
259 <210> SEQ ID NO: 3
260 <211> LENGTH: 33

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261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
266     primer
268 <400> SEQUENCE: 3
269 gtcgtatcat atgtcagcag cagaggaaga aac 33
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273 <211> LENGTH: 32
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
279     primer
281 <400> SEQUENCE: 4
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285 <210> SEQ ID NO: 5
286 <211> LENGTH: 391
287 <212> TYPE: DNA
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
292     Pet15S construct
294 <220> FEATURE:
295 <221> NAME/KEY: CDS
296 <222> LOCATION: (108)..(170)
298 <400> SEQUENCE: 5
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301 ttcccctcta gaaataattt tgtttaactt taagaaggag atataacc atg ggc agc 116
302                                     Met Gly Ser
303                                     1
305 agc cat cat cat cat cat cac agc agc ggc ctg gtg ccg cgc ggc agc 164
306 Ser His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
307     5             10             15
309 cat atg ggatccggaa ttcaaaggcc tacgtcgact agagcctgca gtctcgacca 220
310 His Met
311 20
313 tcatcatcat catcattaat aaaagggcga attccagcac actggcggcc gttactagt 280
315 gatccggctg ctaacaaagc ccgaaaggaa gctgagttgg ctgctgccac cgctgagcaa 340
317 taactagcat aacccttgg ggcctctaaa cgggtcttga ggggtttttt g 391
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321 <211> LENGTH: 21
322 <212> TYPE: PRT
323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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329 <400> SEQUENCE: 6
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VERIFICATION SUMMARY

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